

UNITED STATES PATENT AND TRADEMARK OFFICE  
CERTIFICATE OF CORRECTION

PATENT NO. : 7,250,165 B2  
APPLICATION NO. : 09/920137  
DATED : July 31, 2007  
INVENTOR(S) : Heavner et al.

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It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column 73

Line 21, delete the entire sequence listing through column 84, line 19, and insert

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SEQUENCE LISTING

```
<210> 1
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> Heavy Chain complementarity determinng region 1 (CDR1) .
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<400> 1

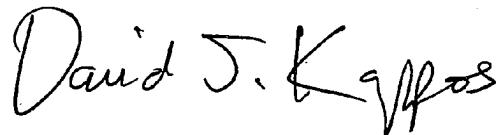
Ser Tyr Ala Met His

1

5

Signed and Sealed this

Tenth Day of August, 2010



David J. Kappos  
*Director of the United States Patent and Trademark Office*

**CERTIFICATE OF CORRECTION (continued)**  
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<210> 2  
<211> 17  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE  
<222> (1)..(17)  
<223> Heavy Chain complementarity determining region 2 (CDR2).

<220>  
<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> Xaa at position 1 is selected from Ile, Phe or Val.

<220>  
<221> MISC\_FEATURE  
<222> (2)..(2)  
<223> Xaa at position 2 is selected from Ile or Met.

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<220>  
<221> MISC\_FEATURE  
<222> (3)..(3)  
<223> Xaa at position 3 is selected from Ser or Leu.

<220>  
<221> MISC\_FEATURE  
<222> (4)..(4)  
<223> Xaa at position 4 is selected from Tyr or Phe.

<220>  
<221> MISC\_FEATURE  
<222> (10)..(10)  
<223> Xaa at position 10 is selected from Lys or Tyr.

<220>  
<221> MISC\_FEATURE  
<222> (11)..(11)  
<223> Xaa at position 11 is selected from Ser or Tyr.

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<220>  
<221> MISC\_FEATURE  
<222> (17) . . . (17)  
<223> Xaa at position 17 is selected from Asp or Gly.

<400> 2

Xaa Xaa Xaa Xaa Asp Gly Ser Asn Lys Xaa Xaa Ala Asp Ser Val Lys Xaa  
1 5 10 15

<210> 3  
<211> 17  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE  
<222> (1) . . . (17)  
<223> Heavy Chain complementarity determinng region 3 (CDR3).

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<220>  
<221> MISC\_FEATURE  
<222> (4)..(4)  
<223> Xaa at position 4 is selected from Ile or Val.

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> Xaa at position 5 is selected from Ser, Ala or Gly.

<220>  
<221> MISC\_FEATURE  
<222> (9)..(9)  
<223> Xaa at position 9 is selected from Asn or Tyr.

<400> 3

Asp	Arg	Gly	Xaa	Xaa	Ala	Gly	Gly	Xaa	Tyr	Tyr	Tyr	Tyr	Gly	Met	Asp	Val
1					5					10					15	

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<210> 4  
<211> 11  
<212> PRT  
<213> Homo sapiens  
  
<220>  
<221> MISC\_FEATURE  
<222> (1)..(11)  
<223> Light Chain complementarity determinng region 1 (CDR1).

<220>  
<221> MISC\_FEATURE  
<222> (7)..(7)  
<223> Xaa at position 7 is selected from Ser or Tyr.

<400> 4

Arg Ala Ser Gln Ser Val Xaa Ser Tyr Leu Ala  
1 5 10

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<210> 5  
<211> 7  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE  
<222> (1)..(7)  
<223> Light Chain complementarity determinng region 2 (CDR2).

<400> 5

Asp Ala Ser Asn Arg Ala Thr

1                      5

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<210> 6

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (1)..(10)

<223> Light Chain complementarity determinng region 3 (CDR3).

<400> 6

Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr

1

5

10

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<210> 7  
<211> 126  
<212> PRT  
<213> Homo sapiens  
<400> 7

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Val  
35 40 45

Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Tyr Gly  
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 8

<211> 108

<212> PRT

<213> Homo sapiens

<400> 8

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Ser Tyr  
20 25 30

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro  
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
100 105

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<210> 9  
<211> 157  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE  
<222> (1)..(157)  
<223> human TNF alpha monomer sequence

<400> 9

Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val  
1 5 10 15

Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg  
20 25 30

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu  
35 40 45

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Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe  
50 55 60

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile  
65 70 75 80

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala  
85 90 95

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys  
100 105 110

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys  
115 120 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe  
130 135 140

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Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
145                    150                    155

<210> 10

<211> 18

<212> DNA

<213> Homo sapiens

<400> 10

ttggtccagt cggactgg                    18

<210> 11

<211> 18

<212> DNA

<213> Homo sapiens

<400> 11

cacctgcact cggtgctt                    18

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<210> 12  
<211> 30  
<212> DNA  
<213> Homo sapiens

<400> 12

cactgttttg agtgtgtacg ggcttaagtt 30

<210> 13  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 13

gccgcacgtg tggaaagg 18

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<210> 14  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 14

agtcaaggc ggactggctt aagtt 25

<210> 15  
<211> 28  
<212> DNA  
<213> Homo sapiens

<400> 15

gttgtccctt ctcacaatct tcgaaattt 28

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<210> 16  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 16

ggcggttagac tactcgtc 18

<210> 17  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 17

Met Asp Trp Thr Trp Ser Ile  
1 5

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<210> 18  
<211> 35  
<212> DNA  
<213> Homo sapiens

<400> 18

tttcgtacgc caccatggac tggacctgga gcatac 35

<210> 19  
<211> 34  
<212> DNA  
<213> Homo sapiens

<400> 19

tttcgtacgc caccatgggg ttggggctga gctg 34

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<210> 20

<211> 35

<212> DNA

<213> Homo sapiens

<400> 20

tttcgtacgc caccatggag tttgggctga gcatg 35

<210> 21

<211> 35

<212> DNA

<213> Homo sapiens

<400> 21

tttcgtacgc caccatgaaa cacctgtggc tcttc 35

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<210> 22  
<211> 35  
<212> DNA  
<213> Homo sapiens

<400> 22

tttcgtacgc caccatgggg tcaaccgcca tcctc 35

<210> 23  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 23

Thr Val Thr Val Ser Ser  
1 5

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<210> 24  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 24

gtgccagttt cagaggagtc cattcaagct taagtt 36

<210> 25  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 25

Met Asp Met Arg Val  
1 5

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<210> 26

<211> 31

<212> DNA

<213> Homo sapiens

<400> 26

tttgcgaca ccatggacat gagggtcctc c

31

<210> 27

<211> 28

<212> DNA

<213> Homo sapiens

<400> 27

tttgcgaca ccatggaaagc cccagctc

28

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<210> 28  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 28

Thr Lys Val Asp Ile Lys

1                       5

<210> 29  
<211> 41  
<212> DNA  
<213> Homo sapiens

<400> 29

ctggtttcac ctatagtttg cattcagaat tcggcgccctt t

41

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<210> 32  
<211> 19  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE  
<222> (1)..(19)  
<223> Signal sequence for heavy chain variable region sequences as presented in original Figure 4

<400> 32

Met	Gly	Phe	Gly	Leu	Ser	Trp	Val	Phe	Leu	Val	Ala	Leu	Leu	Arg	Gly
1															15
Val Gln Cys															

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<210> 33

<211> 20

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (1)..(20)

<223> Signal sequence for light chain variable region sequences as presented in  
original Figure 5

<400> 33

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro

1

5

10

15

Asp Thr Thr Gly

20

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<210> 34

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(421)

<223> heavy chain variable region DNA sequences as presented in original Figure 2A-2B

<400> 34

atggggtttg ggctgagctg ggttttcctc gttgctctt taagagggtgt ccagtgtcag 60  
gtgcagctgg tggagtctgg gggaggcggtg gtccagctg ggaggtccct gagactctcc 120  
tgtgcagccct ctgggttcacc ttcaagtagct atgctatgca ctgggtccgc caggctccgg 180  
caaggggctg gagtgggtgg cagttataatc atatgatgga aaataaaatac tacgcagact 240  
ccgtgaaggg ccgattcacc atctagagac aattccaaga acacgctgtta tctgcaaatg 300  
aacagccaga gctgaggaca cggctgtgttta ttactgtgcg agagatcgag gtatatcagc 360  
aggtgttggata ctactactac tacggtatgg acgtctgggg qcaagggacc acggtcaccc 420  
tctcctca

428

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<210> 35

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(387)

<223> light chain variable region DNA sequences as presented in original Figure 3

<400> 35

atggaagccc cagctcagct tctcttcctc ctgtactct ggctccaga taccaccgga 60  
gaaatttgt tgacacagtc tccagccacc ctgtcttgtt ctccagggg aagagccacc 120  
ctctcctgca gggccagtca gagtgtagc agctacttag cctggtacca acagaaaacct 180  
ggccaggctc ccaggctcct catctatgtat gcatccaaca gggccactgg catcccagcc 240  
aggttcagtg gcagtgggtc tgggacagac ttcaactctca ccatcagcag cctagagcct 300  
gaagatttg cagtttatta ctgtcagcag cgttagcaact ggcctccatt cactttcggtc 360  
cctgggacca aagtggatat caaacgt 387

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